

D. GORZO

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#9

1636

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/145,916

DATE: 07/18/2000
TIME: 13:58:11

Input Set : A:\Bis-039
Output Set: N:\CRF3\07182000\I145916.raw

SEQUENCE LISTING

1 (1) GENERAL INFORMATION:
2 (i) APPLICANT: Simons, Michael
3 Volk, Rudiger
4 Horowitz, Arie
5 (ii) TITLE OF INVENTION: Stimulation of angiogenesis
6 via enhanced endothelial expression of syndecan-4
7 core proteins

8 (iii) NUMBER OF SEQUENCES: 16

9 (iv) CORRESPONDENCE ADDRESS:

10 (A) ADDRESSEE: David Prashker, Esq.
11 (B) STREET: P.O. Box 5387
12 (C) CITY: Magnolia
13 (D) STATE: Massachusetts
14 (E) COUNTRY: USA
15 (F) ZIP: 01930

16 (v) COMPUTER READABLE FORM:

17 (A) MEDIUM TYPE: Diskette, 3.50 inch, 1.40 Mb storage
18 (B) COMPUTER: IBM PS/1
19 (C) OPERATING SYSTEM: MS DOS
20 (D) SOFTWARE: WordPerfect version 5.1

C--> 21 (vi) CURRENT APPLICATION DATA:

C--> 22 (A) APPLICATION NUMBER: US/09/145,916
C--> 23 (B) FILING DATE: 02-Sep-1998
24 (C) CLASSIFICATION: Unknown

25 (vii) ATTORNEY/AGENT INFORMATION:

26 (A) NAME: David Prashker, Esq.
27 (B) REGISTRATION NUMBER: 29,693
28 (C) REFERENCE/DOCKET NUMBER: BIS-039

29 (ix) TELECOMMUNICATION INFORMATION:

30 (A) TELEPHONE: (978) 525-3794

31 (2) INFORMATION FOR SEQ ID NO: 1:

32 (i) SEQUENCE CHARACTERISTICS:

33 (A) LENGTH: 762 base pairs
34 (B) TYPE: nucleic acid
35 (C) STRANDEDNESS: single
36 (D) TOPOLOGY: linear

37 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

39 ATGAGACGTC CGGCCCTCTG CCTTGGCTC TCGCGCCTGG CGCTGCCCT GCAGCCTGCC 60
40 CTCCCCCAA TTGTCAACCGC AAATGTGCTC CCTGAAGACCA AGATGGCTC TGGGACGAC 120
41 TCAGACAAC TCTCTGGCTC AGGCACAGGT GCTTGCCAG ATATGACTTT GTCACGGCAG 180
42 ACACCTTCCA CTTGGAAGGA TGTGTGGCTC CTGACAGCTA CACCCACAGC TCCAGAACCC 240
43 ACCAGCAGGG ATACCGAGGC CACCCCTCACC TCTATCCTGC CGGCTGGAGA GAAGCCTGAG 300
44 GAGGGAGAGC CCGTGGCCA CGTGAAGCA GACGCTGACT TCACGTGCTCG GGACAAGGAG 360
45 AAGGGAGGCC CCACCAAGGCC TAGGGAGACCA ACACAGCTCC CAGTCACCCA ACAGGCCTCA 420
46 ACAGCAGCCA GAGCCACCCAC GGCCCAAGCCA TCTGTCACGT CTCACTCCCCA CGGGGATGTG 480
47 CAACCTGGCC TCCACGAGAC CTTGGCTCCC ACAGCACCCG GCCAACCTGA CCATCAGCCT 540

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RECEIVED

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TECH CENTER 1600/2900

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Input Set : A:\Bis-039
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48 CCAAGTGTGG AGGATGGAGG CACTTCTGTC ATCAAAGAGG TTGTGGAGGA TGAAACTACC 600
 49 AATCAGCTTC CTGCAGGAGA GGGCTCTGGA GAACAAGACT TCACCTTGAA AACATCTGGG 660.
 50 GAGAACACAG CTGTCGCTGG CGTCGAGCCT GACCTTCGGA ATCAGTCCCC AGTGGATGAA 720
 51 GGAGCACACAG GTGCTTCTCA GGGCCTTTG GACAGGAAGG AA 762
 53 (2) INFORMATION FOR SEQ ID NO: 2:
 54 (i) SEQUENCE CHARACTERISTICS:
 55 (A) LENGTH: 1020 base pairs
 56 (B) TYPE: nucleic acid
 57 (C) STRANDEDNESS: single
 58 (D) TOPOLOGY: linear
 59 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 61 GGCAGGAGGG AGGGAGCCAG AGGGAAAAGAA GAGGAGGAGA AGGAGGAGGA CCCGGGGAGG 60
 62 GAGGCCGGG CGGGAGGAG GAGGGGGCA GCGGGGGAGC CAGTGGCCCC GCTTGGAGGC 120
 63 GCTGCTCTCC AGATACCCCCC GGAGCTCCAG CGCGCGGGAT CGCGCGCTCC CGCCGCTCTG 180
 64 CCCCTAAACT TCTGCCGTAG CTCCCTTTCA AGCCAGCGAA TTTATTCCTT AAAACCAGAA 240
 65 ACTGAAACCTC GGCACCGGAA AGGAGTCGGC GGAGGAGGCAA AACCAACAGCA GAGCAAGAAG 300
 66 AGCTTCAGAG AGCAGCCTTC CGGGAGCACC AACTCCGTGT CGGGAGTGCA GAAACCAACA 360
 67 AGTCAGAGGG CGCCGGGTTC CGGGGGCCA GCTCGGGGGC GCGGGAGCAG GCGCAGGAGG 420
 68 AGGAAGCGAG CGCCCCCGAG CCCCAGCCC GAGTCCCCGA GCCTGAGCCG CAATCGCTGC 480
 69 GGTACTCTGC TCCGGATTCTG TGTCGCGGG CTCGCGAGC GCTGGCAGG AGGCTTCGTT 540
 70 TTGCCCCCTGGT TGCAAGCAGC GGCTGGAGC AGCCGGTCCC TGGGAATAT GCGGCGCCGG 600
 71 TGGATCTCTGC TCACCTTGCG CTTGGTGGCC TGCGTGTGCG CGGAGTCGAG AGCAGAGCTG 660
 72 ACATCTGATA AAGACATGTA CCTTGACAAAC AGCTCCATTG AAGAAGCTTC AGGAGTGTAT 720
 73 CCTATTGATG ACGATGACTA CGCTTCTGCG TCTGGCTCGG GAGCTGATGA GGATGTTAGAG 780
 74 AGTCCAGAGC TGACAACAAAC TCGACCAACTT CCAAAGATAC TGTTGACTAG TGCTGCTCCA 840
 75 AAAGTGGAAA CCACGACGCT GAATATACAG AACAAAGATAC CTGCTCAGAC AAAGTCACCT 900
 76 GAAGAAACTG ATAAGAGAA AGTCACTTC TCTGACTCGAG AAAGGAAAAT GGACCCAGCC 960
 77 GAAGAGGATA CAAATGTGTA TACTGAGAAA CACTCAGACAC GTCTGTTAA ACGGACAGAA 1020
 79 (2) INFORMATION FOR SEQ ID NO: 3:
 80 (i) SEQUENCE CHARACTERISTICS:
 81 (A) LENGTH: 340 amino acids
 82 (B) TYPE: amino acid
 83 (C) STRANDEDNESS: single
 84 (D) TOPOLOGY: linear
 85 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
 87 Gly Arg Arg Glu Gly Ala Arg Gly Lys Glu Glu Glu Lys Glu Glu
 88 1 5 10 15
 89 Asp Pro Gly Arg Glu Ala Arg Arg Gly Arg Arg Arg Gly Ala Ala Ala
 90 20 25 30
 91 Glu Pro Val Ala Pro Leu Gly Arg Ala Ala Leu Gln Ile Pro Pro Glu
 92 35 40 45
 93 Leu Gln Pro Arg Gly Ser Arg Ala Pro Ala Ala Leu Pro Leu Asn Phe
 94 50 55 60
 95 Cys Arg Ser Ser Leu Ser Ser Gln Arg Ile Tyr Ser Leu Lys Pro Glu
 96 65 70 75 80
 97 Thr Glu Pro Arg His Gly Lys Gly Val Arg Gly Gly Ala Lys Pro Gln
 98 85 90 95
 99 Gln Ser Lys Lys Ser Phe Arg Glu Gln Pro Ser Arg Ser Thr Asn Ser
 100 100 105 110

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101 Val Ser Gly Val Gln Lys Pro Thr Ser Glu Arg Ala Pro Arg Ser Arg
 102 115 120 125
 103 Gly Ala Ala Ala Gly Gly Gly Ser Arg Arg Arg Arg Arg Lys Arg Ala
 104 130 135 140
 105 Pro Pro Ser Pro Glu Pro Glu Ser Pro Ser Leu Ser Arg Asn Arg Cys
 106 145 150 155 160
 107 Gly Thr Leu Leu Arg Ile Arg Val Arg Gly Leu Ala Glu Arg Trp Ala
 108 165 170 175
 109 Gly Gly Phe Val Leu Pro Trp Leu Gln Ala Ala Ala Gly Ser Ser Arg
 110 180 185 190
 111 Ser Leu Gly Asn Met Arg Arg Ala Trp Ile Leu Leu Thr Leu Gly Leu
 112 195 200 205
 113 Val Ala Cys Val Ser Ala Glu Ser Arg Ala Glu Leu Thr Ser Asp Lys
 114 210 215 220
 115 Asp Met Tyr Leu Asp Asn Ser Ser Ile Glu Glu Ala Ser Gly Val Tyr
 116 225 230 235 240
 117 Pro Ile Asp Asp Asp Tyr Ala Ser Ala Ser Gly Ser Gly Ala Asp
 118 245 250 255
 119 Glu Asp Val Glu Ser Pro Glu Leu Thr Thr Thr Arg Pro Leu Pro Lys
 120 260 265 270
 121 Ile Leu Leu Thr Ser Ala Ala Pro Lys Val Glu Thr Thr Thr Leu Asn
 122 275 280 285
 123 Ile Gln Asn Lys Ile Pro Ala Gln Thr Lys Ser Pro Glu Glu Thr Asp
 124 290 295 300
 125 Lys Glu Lys Val His Leu Ser Asp Ser Glu Arg Lys Met Asp Pro Ala
 126 305 310 315 320
 127 Glu Glu Asp Thr Asn Val Tyr Thr Glu Lys His Ser Asp Ser Leu Phe
 128 325 330 335
 129 Lys Arg Thr Glu
 130 340
 132 (2) INFORMATION FOR SEQ ID NO: 4:
 133 (i) SEQUENCE CHARACTERISTICS:
 134 (A) LENGTH: 1079 base pairs
 135 (B) TYPE: nucleic acid
 136 (C) STRANDEDNESS: single
 137 (D) TOPOLOGY: linear
 138 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
 140 GCCCCCGCGC GCTGCTGAGC CGTCCTTGCG GCACGSSGAT GCCCCGGAG CTGGGGGCC 60
 141 TCGCGGTGCT GCTGCTGCTG CTAGCGCCC GCGCAGCGCT GGCTCAGCCG TGGCGCAATG 120
 142 AGAACTACGA GAGGCCGGTG GACCTGGAGG GCTCTGGGA TGATGATCCC TTTGGGGACG 180
 143 ATGAACTGGA TGACATCTAC TCGGGCTCCG GCTCAGGCTA TTTTGAGCAG GAGTCAGGGT 240
 144 TGGAGACAGC GGTCAGCCTC ACCACGGACA CGTCCGTCCC ACTGCCCACC ACGGTGGCCG 300
 145 TGCTGCGTGT CACCTGGTG CAGGCCATGG CAACACCCCT TGAGCTGTC CCCACAGAGG 360
 146 ACACGTCCCC TGAGCAAACA ACCAGCGTCT TGTATATCCC CAAGATAACA GAAGCACCA 420
 147 TGATCCCCAG CTGGAAAACA ACCACCGCCA GTACCAACTGC CAGTGACTCC CCCAGTACCA 480
 148 CCTCCACAC CACCAACCG GCTGCTACCA CCACCAACAC CACCAACCC ATCAGCACCA 540
 149 CTGTGGCCAC CTCCAAGCCC ACCACTACCC AGAGGTTCTT GCCCCCTTT GTCACCAAGG 600
 150 CAGCCACCCAC CGGGGCCACC ACCCTGGAGA CGCCCCACCAC CTCCCATCCCT GAAACCAGTG 660
 151 TCCTGACAGA GGTGACCACA TCACGGCTTG TCCCCCTCCAG CACAGCCAAG CCGAGGTCCC 720

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152 TGCCAAAACC AAGCACTTCC AGGACTGCAG AACCCACGGA AAAAAGCACT GCCTTGCTT 780
 153 CCAGCCCCAC CACGTGCCA CCCACAGAAG CCCCCCAGGT GGAGCCAGGG GAGTTGACGA 840
 154 CAGTCCTCGA CAGTGACCTG GAAGTCCCAA CCAGTAGTGG CCCCAGCGGG GACTTCGAGA 900
 155 TCCAGGAGGA GGAGGAGACA ACTCGTCTG AGCTGGCAA TGAGGTGGTG GCAGTGGTGA 960
 156 CACCACCAAGC AGCACCGGGG CTGGGCAAGA ATGCAGAGCC GGGGCTCATC GACAACACAA 1020
 157 TAGAGTCGGG CAGCTCGGCT GCTCAGCTCC CCCAGAAAAA CATCCTGGAG AGGAAGGAA 1079
 159 (2) INFORMATION FOR SEQ ID NO: 5:
 160 (i) SEQUENCE CHARACTERISTICS:
 161 (A) LENGTH: 447 base pairs
 162 (B) TYPE: nucleic acid
 163 (C) STRANDEDNESS: single
 164 (D) TOPOLOGY: linear
 165 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
 167 ATGGCGCTG TCTGCCTGTT TGCGCCGCTG CTGCTGTTGC TCCTCGGAGG TTTCCCCGTC 60
 168 GCCCCAGGGC AGTCCATTG AGAGACTGAG GTCATAGACC CCCAGGACCT CCTGGAAGGC 120
 169 AGATACCTCT CTGGCTTCC CCGGGACGT GAAGACGCTG GGGGCTTGA GCAGGACTCT 180
 170 GACTTGAGC TGTCGGGTT CGGAGATCTC GATGACACGG AGGAGCCAG GACCTTCCC 240
 171 GAGGTGATTT CACCTTGGT GCCACTAGAT AACACACATCC CCGAGAATGC CCAGCCTGGC 300
 172 ATCCGTGTCC CCTCAGAGCC CAAGGAACTG GAAGAGAATG AGGTCAATTCC CAAAAGGGTC 360
 173 CCCTCCGACG TGGGGATGCA CGATGTGTCC AACAAAGTGT CCATGTCAG CACTTCCCAG 420
 174 GGCAGCAACA TTTTGAAAG AACTGAG 447
 176 (2) INFORMATION FOR SEQ ID NO: 6:
 177 (i) SEQUENCE CHARACTERISTICS:
 178 (A) LENGTH: 1590 base pairs
 179 (B) TYPE: nucleic acid
 180 (C) STRANDEDNESS: single
 181 (D) TOPOLOGY: linear
 182 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
 184 ATGGAGCTCC GGCCCCGAGG CTGGTGGCTG CTGTGGCGG CGGGCGGCGT AGTCGCTTC 60
 185 GCCCGGGGG ACCCCCCCAG CAAGAGCGG AGTCGAGCG AAGTCGGCCA GATCTACGG 120
 186 GCTAAGGGCT TTAGCTGAG CGACGTGCC CAGGAGAGA TCTCGGGAGA GCACCTGCGG 180
 187 ATCTGCCCCC AGGGCTACAC CTGCTGCAAC AGTGAGATGG AGGAGAACCT GGCCAAACAC 240
 188 AGCCGGATGG AGCTGGAGAC CGCACTCCAC GACAGCAGCC GTGCCCTGCA GGCTACACTG 300
 189 GCCACCCAGC TGATGGCAT CGATGACCC TTCCAGCGC TGCTGAATGA CTCGGAGCGT 360
 190 ACAC TGCTTTCC CGGGGCTTT GGGGACCTGT ACACGAGAA CACTCGGCC 420
 191 TTCCGGGACG TGATGCTGA GCTGCGCTC TACTACCGAG GGGCCAACCT ACACCTTGAG 480
 192 GAGACACTGG CCGAGTTCTG GGCAACGGCTG TGCGAGCGTC TCTTCAGCA GCTGCACCCC 540
 193 CAGCTCTGC TGCCCGATGA CTATCTGGAC TGCCCTGGCA AGCAGGAGA GGCACGTGG 600
 194 CGGTTGGGG ATGCCCTCG AGAACTGCGC CTGAGGGCCA CCCGTCTTT TGTGGGCCA 660
 195 CGATCCTTTC TGCAAGGGCTT GGGTGTGGCC AGTGACGTAG TCCGAAAGGT GGCCCAGGTT 720
 196 CCTCTGGCCC CAGAATGTTG TCGGGCTGTC ATGAAGTGG TCTACTGTGC CCATTGCGG 780
 197 GGAGTCCCTG GTGCCCGGCC CTGTCCGAC TATTGCGGAA ATGTCTCAA AGGCTGCC 840
 198 GCCAACCAAGG CCGACCTGGA TGCCGAGTGG AGGAACCTCC TGGACTCCAT GGTGCTCATC 900
 199 ACTGACAAGT TCTGGGGCCC GTCGGGTGCG GAGAATGTCA TTGGCAGTGT GCATATGTGG 960
 200 CTGGCGGAGG CCATCAACGC CCTCCAGGAC AACAGGACA CACTCACAGC TAAGGTCA 1020
 201 CAGGGCTCGC GAAACCCCAA GGTCAATCCC CATGGCTCTG GGCGCTGAGGA GAAGCGTCGC 1080
 202 CGTGGCAAAAC TGCCACTGCA GGAGAAGTCC TCCACAGGTA CTCTGGAAAA GCTGGTCTCT 1140
 203 GAGGCCAAGG CCCAGCTCCG AGACATTCAAG GACTACTGGA TCAGCCTCCC AGGGACACTG 1200
 204 TGTAGTGAGA AGATGCCAT GAGTCTGCC AGCGATGACCC GCTGCTGGAA TGGGATTCC 1260

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205 AAGGGCCGGT ACCTACCTGA GGTGATGGGT GATGGGCTGG CCAACCAGAT CAACAACCC 1320
 206 GAAGTGGAGG TGGACATCAC CAAGCCGGAT ATGACCATCC GGCAGCAGAT CATGCAGCTC 1380
 207 AAGATCATCG CCAACCGTTT ACCTGGCGCC TACGGTGGCA ATGATGTGGA CTTCCAGGAT 1440
 208 GCCAGTGATG ACGGCAGTGG CTCCGGCAGC GGTGGCGGAT GCCCAGATGA CGCCTGTGGC 1500
 209 CGGAGGGTCA GCAAGAAAGAG CTCCAGCTCC CGGACCCCT TGACCCATGC CCTCCCCGGC 1560
 210 TTGTCAGAAC AGGAGGGACA GAAGACCTCG 1590
 212 (2) INFORMATION FOR SEQ ID NO: 7:
 213 (i) SEQUENCE CHARACTERISTICS:
 214 (A) LENGTH: 531 amino acids
 215 (B) TYPE: amino acid
 216 (C) STRANDEDNESS: single
 217 (D) TOPOLOGY: linear
 218 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
 220 Met Glu Leu Arg Ala Arg Gly Trp Trp Leu Leu Cys Ala Ala Ala Ala 15
 221 1 5 10 15
 222 Leu Val Ala Cys Ala Arg Gly Asp Pro Ala Ser Lys Ser Arg Ser Cys
 223 20 25 30
 224 Ser Glu Val Arg Gln Ile Tyr Gly Ala Lys Gly Phe Ser Leu Ser Asp
 225 35 40 45
 226 Val Pro Gln Ala Glu Ile Ser Gly Glu His Leu Arg Ile Cys Pro Gln
 227 50 55 60
 228 Gly Tyr Thr Cys Cys Thr Ser Glu Met Glu Glu Asn Leu Ala Asn His
 229 65 70 75 80
 230 Ser Arg Met Glu Leu Glu Thr Ala Leu His Asp Ser Ser Arg Ala Leu
 231 85 90 95
 232 Gln Ala Thr Leu Ala Thr Gln Leu His Gly Ile Asp Asp His Phe Gln
 233 100 105 110
 234 Arg Leu Leu Asn Asp Ser Glu Arg Thr Leu Gln Asp Ala Phe Pro Gly
 235 115 120 125
 236 Ala Phe Gly Asp Leu Tyr Thr Gln Asn Thr Arg Ala Phe Arg Asp Leu
 237 130 135 140
 238 Tyr Ala Glu Leu Arg Leu Tyr Tyr Arg Gly Ala Asn Leu His Leu Glu
 239 145 150 155 160
 240 Glu Thr Leu Ala Glu Phe Trp Ala Arg Leu Leu Glu Arg Leu Phe Lys
 241 165 170 175
 242 Gln Leu His Pro Gln Leu Leu Leu Pro Asp Asp Tyr Leu Asp Cys Leu
 243 180 185 190
 244 Gly Lys Gln Ala Glu Ala Leu Arg Pro Phe Gly Asp Ala Pro Arg Glu
 245 195 200 205
 246 Leu Arg Leu Arg Ala Thr Arg Ala Phe Val Ala Ala Arg Ser Phe Val
 247 210 215 220
 248 Gln Gly Leu Gly Val Ala Ser Asp Val Val Arg Lys Val Ala Gln Val
 249 225 230 235 240
 250 Pro Leu Ala Pro Glu Cys Ser Arg Ala Val Met Lys Leu Val Tyr Cys
 251 245 250 255
 252 Ala His Cys Arg Gly Val Pro Gly Ala Arg Pro Cys Pro Asp Tyr Cys
 253 260 265 270
 254 Arg Asn Val Leu Lys Gly Cys Leu Ala Asn Gln Ala Asp Leu Asp Ala
 255 275 280 285

VERIFICATION SUMMARY DATE: 07/18/2000
PATENT APPLICATION: US/09/145,916 TIME: 13:58:12

Input Set : A:\Bis-039
Output Set: N:\CRF3\07182000\I145916.raw

L:21 M:220 C: Keyword misspelled or invalid format, [(vi) CURRENT APPLICATION DATA:]
L:22 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:23 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]